



# SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT  
OF THE SIGMA-1 RECEPTOR

<130> 9151-6

<140> US 09/823,069

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<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(579)

<400> 1

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Met	Gln	Trp	Ala	Val	Gly	Arg	Arg	Trp	Ala	Trp	Ala	Ala	Leu	Leu	Leu	
1				5				10					15			

gct	gtc	gca	gcg	gtg	ctg	acc	cag	gtc	gtc	tgg	ctc	tgg	ctg	ggg	acg	96
Ala	Val	Ala	Ala	Val	Leu	Thr	Gln	Val	Val	Trp	Leu	Trp	Leu	Gly	Thr	
			20					25					30			

cag	agc	ttc	gtc	ttc	cag	cgc	gaa	gag	ata	gcg	cag	ttg	gcg	cgg	cag	144
Gln	Ser	Phe	Val	Phe	Gln	Arg	Glu	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Gln	
		35					40					45				

tac	gct	ggg	ctg	gac	cac	gag	ctg	gcc	ttc	tct	cgt	ctg	atc	gtg	gag	192
Tyr	Ala	Gly	Leu	Asp	His	Glu	Leu	Ala	Phe	Ser	Arg	Leu	Ile	Val	Glu	
	50					55					60					

ctg	cgg	cgg	ctg	cac	cca	ggc	cac	gtg	ctg	ccc	gac	gag	gag	ctg	cag	240
Leu	Arg	Arg	Leu	His	Pro	Gly	His	Val	Leu	Pro	Asp	Glu	Glu	Leu	Gln	
65					70				75					80		

tgg	gtg	ttc	gtg	aat	gcg	ggg	ggc	tgg	atg	ggc	gcc	atg	tgc	ctt	ctg	288
Trp	Val	Phe	Val	Asn	Ala	Gly	Gly	Trp	Met	Gly	Ala	Met	Cys	Leu	Leu	
				85				90						95		

cac	gcc	tcg	ctg	tcc	gag	tat	gtg	ctg	ctc	ttc	ggc	acc	gcc	ttg	ggc	336
His	Ala	Ser	Leu	Ser	Glu	Tyr	Val	Leu	Leu	Phe	Gly	Thr	Ala	Leu	Gly	
			100					105					110			

tcc cgc ggc cac tcg ggg gag acg gta gta cac ggg cct ggt gag gca 384  
 Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
 115 120 125

aca gct gtg gag tgg ggg cca aac aca tgg atg gtg gag tac ggc cgg 432  
 Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
 130 135 140

ggc gtc atc cca tcc acc ctg gcc ttc gcg ctg gcc gac act gtc ttc 480  
 Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe  
 145 150 155 160

agc acc cag gac ttc ctc acc ctc ttc tat act ctt cgc tcc tat gct 528  
 Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala  
 165 170 175

cgg ggc ctc cgg ctt gag ctc acc acc tac ctc ttt ggc cag gac cct 576  
 Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Pro  
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tga 579

<210> 2  
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 <212> PRT  
 <213> Homo sapiens

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Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr  
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Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
 35 40 45

Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
 50 55 60

Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
 65 70 75 80

Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu  
 85 90 95

His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
 100 105 110

Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
 115 120 125

Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
 130 135 140

Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe  
 145 150 155 160

Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala  
 165 170 175

Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Pro  
 180 185 190

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<220>  
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 act att atc gca gtg ctg atc cag gcc gcc tgg ttg tgg ctg ggc act 96  
 Thr Ile Ile Ala Val Leu Ile Gln Ala Ala Trp Leu Trp Leu Gly Thr  
 20 25 30  
 caa aac ttc gtc ttc tct aga gaa gaa ata gcg cag ctt gct cga cag 144  
 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
 35 40 45  
 tat gcg ggg ctg gac cat gag ctt gcc ttc tct cgg ctg atc gtg gag 192  
 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
 50 55 60  
 ctg cgg agg ctg cac cca ggc cac gtg ctg ccg gat gag gag ctg cag 240  
 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
 65 70 75 80  
 tgg gta ttt gtg aac gcg ggc ggc tgg atg ggc gcc atg tgt att ctg 288  
 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu  
 85 90 95  
 cac gcc tcg ctg tct gag tac gtg ctg ctc ttc ggc acc gcc ctg ggc 336  
 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
 100 105 110  
 tcc cat ggc cat tcg gga gag aca gtt gta cac ggg cct gga gaa gca 384  
 Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
 115 120 125

acg gct ctg gag tgg gga cca aac acg tgg atg gtg gag tac ggc cgg 432  
 Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
 130 135 140

ggt gtt att ccg tct acc ctg ttc ttt gca cta gcc gac acc ttc ttc 480  
 Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe  
 145 150 155 160

ggc acc cag gac tac ctc aca ctc ttc tat acc ctt cgg gcc tat gcc 528  
 Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala  
 165 170 175

cgg ggc ctc cgg ctt gag ctt acc acc tac ctc ttt ggc caa gac tcc 576  
 Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Ser  
 180 185 190

tga 579

<210> 4  
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 <400> 4

Met Pro Trp Ala Ala Gly Arg Arg Trp Ala Trp Ile Thr Leu Ile Leu  
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Thr Ile Ile Ala Val Leu Ile Gln Ala Ala Trp Leu Trp Leu Gly Thr  
 20 25 30

Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
 35 40 45

Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
 50 55 60

Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
 65 70 75 80

Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu  
 85 90 95

His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
 100 105 110

Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
 115 120 125

Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
 130 135 140

Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe  
 145 150 155 160

Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala  
 165 170 175

Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Ser  
 180 185 190

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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide primer

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<210> 7  
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Met Gln Trp Ala Val Gly Arg Arg Trp Ala Trp Ala Ala Leu Leu Leu  
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Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr  
 20 25 30

Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
 35 40 45

Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
 50 55 60

Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln



Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
65 70 75 80

Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu  
85 90 95

His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
100 105 110

Ser His Gly His Ser Gly Arg Tyr Trp Ala Glu Ile Ser Asp Thr Ile  
115 120 125

Ile Ser Gly Thr Phe His Gln Trp Lys Glu Gly Thr Thr Lys Ser Glu  
130 135 140

Val Phe Tyr Pro Gly Glu Thr Val Val His Gly Pro Gly Glu Ala Thr  
145 150 155 160

Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg Gly  
165 170 175

Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe Gly  
180 185 190

Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala Arg  
195 200 205

Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Ser  
210 215 220